

Application No.: 09/868577
**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

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For PatentIn software help, call (703) 308-6856

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PCT09

#10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,677

DATE: 04/11/2002

TIME: 16:09:07

Input Set : A:\REG670A.txt

Output Set: N:\CRF3\04112002\I868677.raw

ENTERED

4 <110> APPLICANT: Samuel Davis, Nicholas W. Gale, George D. Yancopoulos, and
 5 Neil Stahl
 7 <120> TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL ACTIVITY OF LIGANDS
 9 <130> FILE REFERENCE: REG 670-A-US
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/868,677
 C--> 12 <141> CURRENT FILING DATE: 2002-02-08
 14 <150> PRIOR APPLICATION NUMBER: PCT/US99/30900
 15 <151> PRIOR FILING DATE: 1999-12-23
 17 <150> PRIOR APPLICATION NUMBER: 60/113,387
 18 <151> PRIOR FILING DATE: 1998-12-23
 20 <160> NUMBER OF SEQ ID NOS: 19
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2058
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)...(2055)
 34 <400> SEQUENCE: 1

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37	1 5 10 15	
39	gac tgt gca gat gta tat caa gct ggt ttt aat aaa agt gga atc tac	96
40	Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr	
41	20 25 30	
43	act att tat att aat aat atg cca gaa ccc aaa aag gtg ttt tgc aat	144
44	Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn	
45	35 40 45	
47	atg gat gtc aat ggg gga ggt tgg act gta ata caa cat cgt gaa gat	192
48	Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp	
49	50 55 60	
51	gga agt cta gat ttc caa aga ggc tgg aag gaa tat aaa atg ggt ttt	240
52	Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe	
53	65 70 75 80	
55	gga aat ccc tcc ggt gaa tat tgg ctg ggg aat gag ttt att ttt gcc	288
56	Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala	
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59	att acc agt cag agg cag tac atg cta aga att gag tta atg gac tgg	336
60	Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp	
61	100 105 110	
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64	Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn	

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71	gga aaa cag agc agc ctg atc tta cac ggt gct gat ttc agc act aaa	480		
72	Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys			
73	145	150	155	160
75	gat gct gat aat gac aac tgt atg tgc aaa tgt gcc ctc atg tta aca	528		
76	Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr			
77	165	170	175	
79	gga gga tgg tgg ttt gat gct tgt ggc ccc tcc aat cta aat gga atg	576		
80	Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met			
81	180	185	190	
83	ttc tat act gcg gga caa aac cat gga aaa ctg aat ggg ata aag tgg	624		
84	Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp			
85	195	200	205	
87	cac tac ttc aaa ggg ccc agt tac tcc tta cgt tcc aca act atg atg	672		
88	His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met			
89	210	215	220	
91	att cga cct tta gat ttt ggc ccc gcg cct ttt aga gac tgt gca gat	720		
92	Ile Arg Pro Leu Asp Phe Gly Pro Ala Pro Phe Arg Asp Cys Ala Asp			
93	225	230	235	240
95	gta tat caa gct ggt ttt aat aaa agt gga atc tac act att tat att	768		
96	Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile			
97	245	250	255	
99	aat aat atg cca gaa ccc aaa aag gtg ttt tgc aat atg gat gtc aat	816		
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103	ggg gga ggt tgg act gta ata caa cat cgt gaa gat gga agt cta gat	864		
104	Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp			
105	275	280	285	
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115	agg cag tac atg cta aga att gag tta atg gac tgg gaa ggg aac cga	1008		
116	Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg			
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119	gcc tat tca cag tat gac aga ttc cac ata gga aat gaa aag caa aac	1056		
120	Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn			
121	340	345	350	
123	tat agg ttg tat tta aaa ggt cac act ggg aca gca gga aaa cag agc	1104		
124	Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser			
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127	agc ctg atc tta cac ggt gct gat ttc agc act aaa gat gct gat aat	1152		
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129	370	375	380	

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139	gga caa aac cat gga aaa ctg aat ggg ata aag tgg cac tac ttc aaa	1296
140	Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys	
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143	ggg ccc agt tac tcc tta cgt tcc aca act atg atg att cga cct tta	1344
144	Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu	
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148	Asp Phe Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys	
149	450 455 460	
151	cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc	1440
152	Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu	
153	465 470 475 480	
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156	Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu	
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159	gtc aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag	1536
160	Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys	
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163	ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag	1584
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165	515 520 525	
167	ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc	1632
168	Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu	
169	530 535 540	
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172	Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys	
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176	Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys	
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179	gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc	1776
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181	580 585 590	
183	cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa	1824
184	Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys	
185	595 600 605	
187	ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag	1872
188	Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln	
189	610 615 620	
191	ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac gcc	1920
192	Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly	
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200 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
201                               660                               665                               670
203 cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga      2058
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217 20 25 30
218 Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn
219 35 40 45
220 Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp
221 50 55 60
222 Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe
223 65 70 75 80
224 Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala
225 85 90 95
226 Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp
227 100 105 110
228 Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn
229 115 120 125
230 Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala
231 130 135 140
232 Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys
233 145 150 155 160
234 Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr
235 165 170 175
236 Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met
237 180 185 190
238 Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp
239 195 200 205
240 His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met
241 210 215 220
242 Ile Arg Pro Leu Asp Phe Gly Pro Ala Pro Phe Arg Asp Cys Ala Asp
243 225 230 235 240
244 Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
245 245 250 255
246 Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
247 260 265 270
248 Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
249 275 280 285

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254 Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
255      325      330      335
256 Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
257      340      345      350
258 Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
259      355      360      365
260 Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
261      370      375      380
262 Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
263 385      390      395      400
264 Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
265      405      410      415
266 Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
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271      450      455      460
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274 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
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277      500      505      510
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281      530      535      540
282 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
283 545      550      555      560
284 Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
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286 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
287      580      585      590
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291      610      615      620
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293 625      630      635      640
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297      660      665      670
298 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:1427 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11